

## Variability and Character Association Analyses in Safflower (*Carthamus tinctorius* L.)

**Key words** : Character Association, Safflower, Variability

Safflower is an important source of healthy oil rich in poly-unsaturated fatty acids. Varietal improvement in safflower mainly depends on genetic variation and association among various component characters with yield and oil content. This study was undertaken to estimate the extent of variation and to establish correlation among various components and their direct and indirect effects on yield in safflower.

The experiment comprising 18 lines of safflower was conducted at Agricultural Research Station, Tandur during *rabi* 2007-08 in a randomized block design with three replications. Recommended agronomic practices with inter- and intra-row spacing of 45cm and 20cm were followed. Data on seven characters were recorded on randomly selected five plants/ plot basis in each replication. Phenotypic and genotypic components of variation were worked out as per Lush (1940). Phenotypic and genotypic correlation coefficients were worked out as per Falconer (1964) and path coefficient analysis as suggested by Dewey and Lu (1959).

The analysis of variance revealed significant differences among the genotypes for seed yield and component characters indicating considerable amount of genetic variation in the material. The phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV) indicating considerable environmental influence on the expression of the traits. High GCV, PCV with high heritability and genetic advance was recorded by number of capitula plant<sup>-1</sup> (20.85%, 25.84%, 65.10 and 8.30) and number of seeds capitulum<sup>-1</sup> (15.76%, 18.14%, 75.50 and 9.25) indicating lesser environmental influence and prevalence of additive gene action in the expression of these traits, hence amenable for simple selection, in accordance with Lakshyadeep *et al.*, (2005) and Beena Nair *et al.*, (2006). High heritability with low genetic advance was recorded by days to 50% flowering (80.11 and 3.36), days to maturity (79.11 and 3.30), 100 seed weight (91.39 and 0.86) and oil content (57.85 and 5.52) indicating preponderance of non-additive gene action in the expression of these traits. Low

heritability for seed yield (33.80) suggested that direct selection for this trait may not be fruitful and indirect selection through other component traits will benefit yield improvement.

Days to 50% flowering and days to maturity showed positive significant association with 100-seed weight (Table 1). Number of capitula plant<sup>-1</sup> showed negative significant association with number of seeds capitulum<sup>-1</sup>. Number of seeds capitulum<sup>-1</sup> recorded negative significant correlation with 100-seed weight and positive association with oil content, in agreement with Dalvi *et al.*, (2005). Positive association of 100 seed weight with seed yield and oil content indicated that seed with more weight possessed more oil content, as also reported by Anjani (2005) and the possibility of simultaneous improvement for both seed yield and oil content.

Path analysis (Table 2) revealed that days to 50% flowering, days to maturity and 100 seed weight recorded positive direct effect resulting in positive association with seed yield as also reported by Dalvi *et al.* (2005) and Bidgoli *et al.*, (2006). Number of capitula plant<sup>-1</sup> and seeds capitulum<sup>-1</sup> showed negative direct effect on seed yield. However, indirect positive effects of these traits were manifested through 100 seed weight resulting in positive association with seed yield. The present study indicated that days to 50% flowering, number of seeds capitulum<sup>-1</sup> and 100 seed weight are the important traits to be considered for yield and oil improvement for the material under study in safflower.

### LITERATURE CITED

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Table 1. Genotypic and phenotypic correlation coefficients between seed yield and its components in safflower (*Carthamus tinctorius* L.).

Character	Days to maturity	Number of capitula plant <sup>-1</sup>	Number of seeds capitulum <sup>-1</sup>	100-seed weight	Oil content	Seed yield
Days to 50% flowering	0.93** (0.98**)	-0.31 (0.31)	-0.12 (-0.13)	0.49* (0.50*)	-0.23 (-0.25)	0.46* (0.57*)
Days to maturity		-0.32 (-0.39)	-0.28 (-0.36)	0.45* (0.52*)	-0.23 (-0.24)	0.46* (0.47*)
Number of capitula plant <sup>-1</sup>			-0.52* (-0.54*)	0.41 (0.44)	-0.39 (-0.32)	0.26 (0.27)
Number of seeds capitulum <sup>-1</sup>				-0.56* (-0.61**)	-0.28 (-0.29)	0.32 (0.45)
100-seed weight					0.49* (0.52*)	0.53* (0.55*)
Oil content						0.05 (0.13)

Figures in parentheses are genotypic estimates; \* = Significant at 5% level;  
\*\* = Significant at 1% level

Table 2. Direct (diagonal) and indirect effects of six characters on seed yield in safflower (*Carthamus tinctorius* L.).

Character	Days to 50% flowering	Days to maturity	Number of capitula plant <sup>-1</sup>	Number of seeds capitulum <sup>-1</sup>	100-seed weight	Oil content (%)	Correlation with seed yield plant <sup>-1</sup>
Days to 50% flowering	<u>0.1125</u> (0.3201)	0.0325 (0.0651)	0.0035 (0.0214)	0.0018 (-0.0017)	0.0058 (0.0062)	0.0021 (0.0132)	0.4695* (0.5728*)
Days to maturity	0.2453 (0.4210)	<u>0.3236</u> (0.4659)	0.0058 (0.0212)	0.0214 (0.0363)	0.0072 (0.0089)	0.0115 (0.0204)	0.4681* (0.4790*)
Number of capitula plant <sup>-1</sup>	0.0157 (0.0417)	0.0585 (0.0699)	<u>-0.0228</u> (-0.0858)	0.0130 (0.0210)	0.0013 (0.0021)	-0.0056 (0.0045)	0.2684 (0.2716)
Number of seeds capitulum <sup>-1</sup>	-0.0214 (0.0102)	-0.0129 (-0.0245)	-0.0054 (-0.0206)	<u>-0.0176</u> (-0.0924)	0.0054 (0.0105)	0.0139 (0.0122)	0.3254 (0.4562)
100-seed weight	0.0206 (0.0105)	0.0527 (0.0634)	0.0010 (0.0005)	0.0045 (0.0202)	<u>0.0415</u> (0.0432)	-0.0123 (-0.0521)	0.5349* (0.5550*)
Oil content	0.0047 (0.0550)	0.0245 (0.0086)	-0.0072 (0.0027)	-0.0012 (-0.0006)	-0.0089 (-0.0140)	<u>0.0423</u> (0.0526)	0.0527 (0.1333)

\* = Significant at 0.05 level; Figures in parentheses are genotypic path values and visit parentheses phenotypic values

Residual effect at phenotypic level: 0.0315; Residual effect at genotypic level = 0.0124

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